IFWO

RAW SEQUENCE LISTING   DATE: 08/20/2004
PATENT APPLICATION: **US/10/774,721**   TIME: 09:06:55

Input Set : **A:\Ser. No. 10 774,721 Sequence Listing.txt**
Output Set: **N:\CRF4\08202004\J774721.raw**

```
   3 <110> APPLICANT: JOCKERS, Ralf
   4        COUTURIER, Cyril
   5        UHLMANN, Eugen
   7 <120> TITLE OF INVENTION: Olignocleotides Which inhibit Expression of the OB-RGRP
Protein
   8        And Method For Detecting Compounds Which Modify The Interaction
   9        Between Proteins Of the OB-RGRP Family And The Leptin Receptor
  11 <130> FILE REFERENCE: FRAV2003/0005 US NP
  13 <140> CURRENT APPLICATION NUMBER: 10/774,721
  14 <141> CURRENT FILING DATE: 2004-02-09
  16 <150> PRIOR APPLICATION NUMBER: 60/461,005
  17 <151> PRIOR FILING DATE: 2003-04-07
  19 <150> PRIOR APPLICATION NUMBER: 0301543
  20 <151> PRIOR FILING DATE: 2003-02-10
  22 <160> NUMBER OF SEQ ID NOS: 47
  24 <170> SOFTWARE: PatentIn version 3.1
  26 <210> SEQ ID NO: 1
  27 <211> LENGTH: 648
  28 <212> TYPE: DNA
  29 <213> ORGANISM: Homo sapiens
  31 <400> SEQUENCE: 1
  32 cactttattc tgattacagt gcattgaatt tcttagaact catactatct gtatacatgt     60
  34 gcacatgcgg cattttacta tgaaatttaa tatgctgggt tttttaatac ctttatatat    120
  36 catgttcact ttaagaaaga cttcataagt aggagatgag ttttattctc agcaaataga    180
  38 cctgtcaaat ttagattatg ttactcaaat tatgttactt gtttggctgt tcatgtagtc    240
  40 acggtgctct cagaaaatat attaacgcag tcttgtaggc agctgccacc ttatgcagtg    300
  42 catcgaaacc ttttgcttgg ggatgtgctt ggagaggcag ataacgctga agcaggcctc    360
  44 tcatgaccca ggaaggccgg ggtggatccc tctttgtgtt gtagtccatg ctattaaaag    420
  46 tgtggcccac agaccaagag cctcaacatt tcctagagcc ttattagaaa tgcagaatct    480
  48 gaagccccac tctggaccca ggacattttg atgagatcca aaggagttgt atgcacatga    540
  50 aagtttgaga agcatcatca tagagaagta aacatcacac ccaacttcct tatctttcca    600
  52 gtggctaaac cacttaacct ctctgggtgt tacctgctca tttgttta                 648
  55 <210> SEQ ID NO: 2
  56 <211> LENGTH: 20
  57 <212> TYPE: DNA
  58 <213> ORGANISM: Artificial Sequence
  60 <220> FEATURE:
  61 <223> OTHER INFORMATION: AS14
  63 <220> FEATURE:
  64 <221> NAME/KEY: misc_feature
  65 <223> OTHER INFORMATION: antisens AS14
  68 <400> SEQUENCE: 2
  69 aatgccgcat gtgcacatgt                                                  20
  72 <210> SEQ ID NO: 3
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Input Set : **A:\Ser. No. 10 774,721 Sequence Listing.txt**
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 73 <211> LENGTH: 396
 74 <212> TYPE: DNA
 75 <213> ORGANISM: Homo sapiens
 77 <220> FEATURE:
 78 <221> NAME/KEY: CDS
 79 <222> LOCATION: (1)..(396)
 80 <223> OTHER INFORMATION:
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W--> 83 <400> 3

```
 84 atg gcg ggc gtt aaa gct ctc gtg gca tta tcc ttc agt ggg gct att        48
 85 Met Ala Gly Val Lys Ala Leu Val Ala Leu Ser Phe Ser Gly Ala Ile
 86 1               5                   10                  15
 88 gga ctg act ttt ctt atg ctg gga tgt gcc tta gag gat tat ggc gtt        96
 89 Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr Gly Val
 90                 20                  25                  30
 92 tac tgg ccc tta ttc gtc ctg att ttc cac gcc atc tcc ccc atc ccc       144
 93 Tyr Trp Pro Leu Phe Val Leu Ile Phe His Ala Ile Ser Pro Ile Pro
 94         35                  40                  45
 96 cat ttc att gcc aaa aga gtc acc tat gac tca gat gca acc agt agt       192
 97 His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser
 98     50                  55                  60
100 gcc tgt cgg gaa ctg gca tat ttc ttc act act gga att gtt gtt tct       240
101 Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr Gly Ile Val Val Ser
102 65                  70                  75                  80
104 gcc ttt gga ttt cct gtt att ctt gct cgt gtg gct gtg atc aaa tgg       288
105 Ala Phe Gly Phe Pro Val Ile Leu Ala Arg Val Ala Val Ile Lys Trp
106                 85                  90                  95
108 gga gcc tgc ggc ctt gtg ttg gca ggc aat gca gtc att ttc ctt aca       336
109 Gly Ala Cys Gly Leu Val Leu Ala Gly Asn Ala Val Ile Phe Leu Thr
110                 100                 105                 110
112 att caa ggg ttt ttc ctt ata ttt gga aga gga gat gat ttt agc tgg       384
113 Ile Gln Gly Phe Phe Leu Ile Phe Gly Arg Gly Asp Asp Phe Ser Trp
114             115                 120                 125
116 gag cag tgg tag                                                        396
117 Glu Gln Trp
118     130
121 <210> SEQ ID NO: 4
122 <211> LENGTH: 131
123 <212> TYPE: PRT
124 <213> ORGANISM: Homo sapiens
126 <400> SEQUENCE: 4
128 Met Ala Gly Val Lys Ala Leu Val Ala Leu Ser Phe Ser Gly Ala Ile
129 1               5                   10                  15
132 Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr Gly Val
133                 20                  25                  30
136 Tyr Trp Pro Leu Phe Val Leu Ile Phe His Ala Ile Ser Pro Ile Pro
137         35                  40                  45
140 His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser
141     50                  55                  60
144 Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr Gly Ile Val Val Ser
```

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Input Set : **A:\Ser. No. 10 774,721 Sequence Listing.txt**
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```
145 65                    70              75               80
148 Ala Phe Gly Phe Pro Val Ile Leu Ala Arg Val Ala Val Ile Lys Trp
149              85              90               95
152 Gly Ala Cys Gly Leu Val Leu Ala Gly Asn Ala Val Ile Phe Leu Thr
153              100             105              110
156 Ile Gln Gly Phe Phe Leu Ile Phe Gly Arg Gly Asp Asp Phe Ser Trp
157         115              120              125
160 Glu Gln Trp
161       130
164 <210> SEQ ID NO: 5
165 <211> LENGTH: 1359
166 <212> TYPE: DNA
167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
170 <223> OTHER INFORMATION: OB RGRP LUC
172 <220> FEATURE:
173 <221> NAME/KEY: misc_feature
174 <223> OTHER INFORMATION: OB RGRP LUC
177 <220> FEATURE:
178 <221> NAME/KEY: CDS
179 <222> LOCATION: (1)..(1359)
180 <223> OTHER INFORMATION:
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W--> `183 <400> 5`
```
184 atg gcg ggc gtt aaa gct ctc gtg gca tta tcc ttc agt ggg gct att   48
185 Met Ala Gly Val Lys Ala Leu Val Ala Leu Ser Phe Ser Gly Ala Ile
186 1               5                   10                  15
188 gga ctg act ttt ctt atg ctg gga tgt gcc tta gag gat tat ggc gtt   96
189 Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr Gly Val
190              20                  25                  30
192 tac tgg ccc tta ttc gtc ctg att ttc cac gcc atc tcc ccc atc ccc  144
193 Tyr Trp Pro Leu Phe Val Leu Ile Phe His Ala Ile Ser Pro Ile Pro
194          35                  40                  45
196 cat ttc att gcc aaa aga gtc acc tat gac tca gat gca acc agt agt  192
197 His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser
198      50                  55                  60
200 gcc tgt cgg gaa ctg gca tat ttc ttc act act gga att gtt gtt tct  240
201 Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr Gly Ile Val Val Ser
202 65                  70                  75                  80
204 gcc ttt gga ttt cct gtt att ctt gct cgt gtg gct gtg atc aaa tgg  288
205 Ala Phe Gly Phe Pro Val Ile Leu Ala Arg Val Ala Val Ile Lys Trp
206              85                  90                  95
208 gga gcc tgc ggc ctt gtg ttg gca ggc aat gca gtc att ttc ctt aca  336
209 Gly Ala Cys Gly Leu Val Leu Ala Gly Asn Ala Val Ile Phe Leu Thr
210              100                 105                 110
212 att caa ggg ttt ttc ctt ata ttt gga aga gga gat gat ttt agc tgg  384
213 Ile Gln Gly Phe Phe Leu Ile Phe Gly Arg Gly Asp Asp Phe Ser Trp
214          115                 120                 125
216 gag cag tgg att ccg ggg gat cca ccg gct aga gcc acc atg acc agc  432
217 Glu Gln Trp Ile Pro Gly Asp Pro Pro Ala Arg Ala Thr Met Thr Ser
```

```
218      130                    135                    140
220 aag gtg tac gac ccc gag cag agg aag agg atg atc acc ggc ccc cag    480
221 Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr Gly Pro Gln
222 145                    150                    155                    160
224 tgg tgg gcc agg tgc aag cag atg aac gtg ctg gac agc ttc atc aac    528
225 Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser Phe Ile Asn
226                    165                    170                    175
228 tac tac gac agc gag aag cac gcc gag aac gcc gtg atc ttc ctg cac    576
229 Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile Phe Leu His
230                    180                    185                    190
232 ggc aac gcc gct agc agc tac ctg tgg agg cac gtg gtg ccc cac atc    624
233 Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val Pro His Ile
234            195                    200                    205
236 gag ccc gtg gcc agg tgc atc atc ccc gat ctg atc ggc atg ggc aag    672
237 Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly Met Gly Lys
238        210                    215                    220
240 agc ggc aag agc ggc aac ggc agc tac agg ctg ctg gac cac tac aag    720
241 Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp His Tyr Lys
242 225                    230                    235                    240
244 tac ctg acc gcc tgg ttc gag ctc ctg aac ctg ccc aag aag atc atc    768
245 Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys Lys Ile Ile
246                    245                    250                    255
248 ttc gtg ggc cac gac tgg ggc gcc tgc ctg gcc ttc cac tac agc tac    816
249 Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His Tyr Ser Tyr
250                    260                    265                    270
252 gag cac cag gac aag atc aag gcc atc gtg cac gcc gag agc gtg gtg    864
253 Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu Ser Val Val
254            275                    280                    285
256 gac gtg atc gag agc tgg gac gag tgg cca gac atc gag gag gac atc    912
257 Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu Glu Asp Ile
258        290                    295                    300
260 gcc ctg atc aag agc gag gag ggc gag aag atg gtg ctg gag aac aac    960
261 Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu Glu Asn Asn
262 305                    310                    315                    320
264 ttc ttc gtg gag acc atg ctg ccc agc aag atc atg aga aag ctg gag   1008
265 Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg Lys Leu Glu
266                    325                    330                    335
268 ccc gag gag ttc gcc gcc tac ctg gag ccc ttc aag gag aag ggc gag   1056
269 Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu Lys Gly Glu
270                    340                    345                    350
272 gtg aga aga ccc acc ctg agc tgg ccc aga gag atc ccc ctg gtg aag   1104
273 Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro Leu Val Lys
274            355                    360                    365
276 ggc ggc aag ccc gac gtg gtg cag atc gtg aga aac tac aac gcc tac   1152
277 Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr Asn Ala Tyr
278        370                    375                    380
280 ctg aga gcc agc gac gac ctg ccc aag atg ttc atc gag agc gac ccc   1200
281 Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu Ser Asp Pro
282 385                    390                    395                    400
```

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```
284 ggc ttc ttc agc aac gcc atc gtg gag ggc gcc aag aag ttc ccc aac        1248
285 Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys Phe Pro Asn
286               405             410             415
288 acc gag ttc gtg aag gtg aag ggc ctg cac ttc agc cag gag gac gcc        1296
289 Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln Glu Asp Ala
290               420             425             430
292 ccc gac gag atg ggc aag tac atc aag agc ttc gtg gag aga gtg ctg        1344
293 Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu Arg Val Leu
294               435             440             445
296 aag aac gag cag taa                                                     1359
297 Lys Asn Glu Gln
298       450
301 <210> SEQ ID NO: 6
302 <211> LENGTH: 452
303 <212> TYPE: PRT
304 <213> ORGANISM: Artificial Sequence
306 <220> FEATURE:
307 <223> OTHER INFORMATION: OB RGRP LUC
309 <220> FEATURE:
310 <221> NAME/KEY: misc_feature
311 <223> OTHER INFORMATION: OB RGRP LUC
313 <400> SEQUENCE: 6
315 Met Ala Gly Val Lys Ala Leu Val Ala Leu Ser Phe Ser Gly Ala Ile
316 1               5               10              15
319 Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr Gly Val
320               20              25              30
323 Tyr Trp Pro Leu Phe Val Leu Ile Phe His Ala Ile Ser Pro Ile Pro
324               35              40              45
327 His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser
328       50              55              60
331 Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr Gly Ile Val Val Ser
332 65              70              75              80
335 Ala Phe Gly Phe Pro Val Ile Leu Ala Arg Val Ala Val Ile Lys Trp
336               85              90              95
339 Gly Ala Cys Gly Leu Val Leu Ala Gly Asn Ala Val Ile Phe Leu Thr
340               100             105             110
343 Ile Gln Gly Phe Phe Leu Ile Phe Gly Arg Gly Asp Asp Phe Ser Trp
344               115             120             125
347 Glu Gln Trp Ile Pro Gly Asp Pro Pro Ala Arg Ala Thr Met Thr Ser
348       130             135             140
351 Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr Gly Pro Gln
352 145             150             155             160
355 Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser Phe Ile Asn
356               165             170             175
359 Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile Phe Leu His
360               180             185             190
363 Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val Pro His Ile
364               195             200             205
367 Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly Met Gly Lys
```

VERIFICATION SUMMARY   DATE: 08/20/2004
PATENT APPLICATION: **US/10/774,721**   TIME: 09:06:56

Input Set : **A:\Ser. No. 10 774,721 Sequence Listing.txt**
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L:83 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:80
L:183 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:180
L:450 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:447
L:669 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:666
L:1147 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:1144
L:1814 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:1811
L:2433 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:2430
L:2530 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:2527
L:2794 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:2791